CLEAN VERSION OF AMENDMENTS

IN THE CLAIMS

Please cancel claims 1-2, 4-7 and 11.

Please introduce new claims 12-23, which read as follows:

12. (newly added) A method for altering the substrate specificity of an enzyme to a substrate from a substrate specificity where catalysis does not occur to a substrate specificity where catalysis does occur, comprising the steps of:

a) introducing a DNA sequence coding for the enzyme into the *Escherichia coli* strain XL1-Red or into a functional derivative thereof,

b) incubating the transformed *Escherichia coli* strain XL1-Red or its functional derivative to generate mutations in the DNA sequence,

c) transferring the mutated DNA sequence from the transformed *Escherichia coli* strain XL1-Red or its functional derivative to a microorganism which has no impeding enzyme activity,

d) incubating this microorganism to detect the enzyme activity in at least one selection medium which comprises at least one enzyme substrate to recognize altered substrate specificity of the enzyme, with or without other indicator substances,

e) selecting the microorganisms which show an alteration in the substrate specificity, said microorganisms in steps b), d) and e) being a member selected from the group consisting of bacteria, fungi and yeasts,

wherein the enzyme is selected from the group consisting of lipases, amidases,

nitrilases, ether hydrolases, peroxidases, glycosidases and phytases.

13. (newly added) The method of claim 12, wherein the enzyme is a lipase.

14. (newly added) The method of claim 12, wherein the enzyme is an amidase.

15. (newly added) The method of claim 12, wherein the enzyme is a nitrilase.

16. (newly added) The method of claim 12, wherein the enzyme is an ether hydrolase.

17. (newly added) The method of claim 12, wherein the enzyme is a peroxidase.

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18. (newly added) The method of claim 12, wherein the enzyme is a glycosidase.

19. (newly added) The method of claim 12, wherein the enzyme is a phytase.

20. (newly added) The method of claim 13, wherein the lipase is selected from the group of lipases consisting of *Pseudomonas cepacia* lipase PS, *Pseudomonas cepacia* lipase AH, acylase, *Rhizopus delamar* lipase, *Rhizopus javanicus* lipase, *Candida rugosa* lipase, *Mucor javanicus* lipase, *Penicillium roquefortii* lipase, *Penicillium cyclopium* lipase, *Chromobacterium viscosum* lipase, *Rhizomucor*

miehei lipase, *Humicola lanuginosa* lipase, *Candida antarctica* lipase B and *Candida antarctica* lipase A.

21. (newly added) The method of claim 12, wherein steps (a) to (e) are performed several times in sequence by reisolating and retransforming the DNA sequence from the microorganisms selected in step (e) to the strain *Escherichia coli* XL-1 Red or its functional derivative.

22. (newly added) A method for altering the substrate specificity of an enzyme to a substrate from a substrate specificity where catalysis does not occur to a substrate specificity where catalysis does occur, comprising the steps of:

a) introducing a DNA sequence coding for the enzyme into the *Escherichia coli* strain XL1-Red or into a functional derivative thereof,

b) incubating the transformed *Escherichia coli* strain XL1-Red or its functional derivative to generate mutations in the DNA sequence,

c) transferring the mutated DNA sequence from the transformed *Escherichia coli* strain XL1-Red or its functional derivative to a microorganism which has no impeding enzyme activity,

d) incubating this microorganism to detect the enzyme activity in at least one selection medium which comprises at least one enzyme substrate to recognize altered substrate specificity of the enzyme, with or without other

indicator substances,

e) selecting the microorganisms which show an alteration in the substrate specificity, said microorganisms in steps b), d) and e) being a member selected from the group consisting of bacteria, fungi and yeasts,

wherein the enzyme is an esterase selected from the group consisting of *Pseudomonas fluorescens* esterase, pig liver esterase and *Thermoanaerobium brockii* esterase.

23. (newly added) The method of claim 22, wherein steps (a) to (e) are performed several times in sequence by reisolating and retransforming the DNA sequence from the microorganisms selected in step (e) to the strain *Escherichia coli* XL-1 Red or its functional derivative.